

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:40:09 ON 06 APR 2001
L1 406 SEA PLU=ON (TRANSGENIC) AND (PLANT OR TOBACCO OR BARLEY OR
RICE OR BRASSICA OR PICEA OR SOYBEAN) AND (DIGEST?)
D KWIC
L2 258 SEA PLU=ON L1 NOT PY>1998
L3 172 DUP REM L2 (86 DUPLICATES REMOVED)
D KWIC
L4 19 SEA PLU=ON L3 AND (DIGEST?)/TI
D TI 1-19
D IBIB AB 4

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:46:35 ON 06 APR 2001
L5 97 SEA PLU=ON (TRANSGENIC) AND (PLANT OR TOBACCO OR BARLEY OR
RICE OR BRASSICA OR PICEA OR SOYBEAN) AND (ALLERGEN?)
L6 61 SEA PLU=ON L5 NOT PY>1998
L7 36 SEA PLU=ON L6 AND ALLERGEN?/TI
L8 30 DUP REM L7 (6 DUPLICATES REMOVED)
D TI 1-30

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:52:18 ON 06 APR 2001
L10 2 SEA PLU=ON L9
D TI 1-2
D IBIB AB 1-2
L11 6052 SEA PLU=ON THIOREDOXIN
L12 142 SEA PLU=ON THIOREDOXIN H
L13 13 SEA PLU=ON L12 AND (TRANSGENIC)
L14 8 DUP REM L13 (5 DUPLICATES REMOVED)
D TI 1-8
D IBIB AB 1-8

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 16:01:29 ON 06 APR 2001
L16 0 SEA PLU=ON L15
L17 8 SEA PLU=ON (TRXH? OR THIOH?) AND (TRANSGENIC)
L18 3 SEA PLU=ON L17 NOT L13
L19 3 DUP REM L18 (0 DUPLICATES REMOVED)
D IBIB AB 1-3
D IBIB AB 1-3
L20 50 SEA PLU=ON (THIOREDOXIN) AND (EXPRESS? OR TRANSFORM? OR
INTRODUCE?) (3A) (PLANT OR TOBACCO OR RICE OR BARLEY OR MAIZE
OR
WHEAT OR RYE OR SORGHUM OR MILLET OR TRITICALE OR FORAGE)
L21 44 SEA PLU=ON L20 NOT (L13)
L22 26 SEA PLU=ON L21 NOT PY>1998
L23 17 DUP REM L22 (9 DUPLICATES REMOVED)
L24 4 SEA PLU=ON L23 AND (THIOREDOXIN H)
L25 0 SEA PLU=ON L23 AND (THIOH? OR TRXH?)
L26 4 DUP REM L24 (0 DUPLICATES REMOVED)
D IBIB AB 1-4

Cham

(FILE 'HOME' ENTERED AT 17:06:32 ON 06 APR 2001)

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 17:06:42 ON 06 APR 2001
L1 0 S TRANSGENIC AND (PLANT OR RICE OR BARLEY OR TOBACCO OR MAIZE
O
L2 13 S TRANSGENIC AND (PLANT OR RICE OR BARLEY OR TOBACCO OR MAIZE
O
L3 11 DUP REM L2 (2 DUPLICATES REMOVED)

FILE

L Number	Hits	Search Text	DB	Time stamp
1	127	((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage) and (allergen\$6) (allergen\$6 near5 (reduc\$4 alter\$3 decreas\$3)))	USPAT	2001/04/06 16:41
2	368	((allergen\$6 near5 (reduc\$4 alter\$3 decreas\$3))) and ((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage) and (allergen\$6))	USPAT	2001/04/06 16:22
3	15	((allergen\$6 near5 (reduc\$4 alter\$3 decreas\$3))) and ((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage) and (allergen\$6))	USPAT	2001/04/06 16:44
4	33	((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage) and (earl\$3 near3 (germinat\$3 amylase)))	USPAT	2001/04/06 16:54
5	22	((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage) and ((earl\$3 increas\$3) near3 (pullulanase amylase)))	USPAT	2001/04/06 17:04
6	0	((transgenic) same pullulanase) and (plant tobacco rice barley maize wheat rye sorghum millet triticales forage)	USPAT	2001/04/06 17:05

L1 ANSWER 13 OF 14 AGRICOLA

ACCESSION NUMBER: 93:34770 AGRICOLA

DOCUMENT NUMBER: IND93018147

TITLE: Specific reduction of wheat storage proteins by
thioredoxin h.

AUTHOR(S): Kobrehel, K.; Wong, J.H.; Balogh, A.; Kiss, F.; Yee,
B.C.; Buchanan, B.B.

CORPORATE SOURCE: INRA, Montpellier, France

AVAILABILITY: DNAL (450 P692)

SOURCE: Plant physiology, July 1992. Vol. 99, No. 3. p.
919-924

Publisher: Rockville, Md. : American Society of Plant
Physiologists.

CODEN: PLPHAY; ISSN: 0032-0889

NOTE: Includes references.

DOCUMENT TYPE: Article

FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension

LANGUAGE: English

AB Gliadins and glutenins, the major storage proteins of wheat endosperm (*Triticum durum*, Desf. cv Monroe), were reduced in vitro by the NADP/thioredoxin system (NADPH, NADP-thioredoxin reductase and thioredoxin; in plants, the h type) from either the same source or the bacterium *Escherichia coli*. A more limited reduction of certain members of these protein groups was achieved with the reduced form of glutathione or glutaredoxin, a protein known to replace thioredoxin in certain bacterial and mammalian enzyme systems but not known to occur in higher plants. Endosperm extracts contained the enzymes necessary to reduce NADP by the oxidative pentose phosphate pathway (hexokinase, glucosephosphate 6-dehydrogenase, 6-phosphogluconate dehydrogenase). The gliadins and glutenins were also reduced in vivo during germination--an event that accompanied their proteolytic breakdown. The results suggest that thioredoxin, reduced by NADPH generated via the oxidative pentose phosphate pathway, functions as a signal in germination to enhance metabolic processes such as the mobilization of storage proteins and, as found earlier, the activation of enzymes.

HITS AT: 37-75

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L11 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2002 ACS

RN 163539-45-5 REGISTRY

CN DNA (barley clone Hor3-1 gene Hor3 fragment plus 5'-flank) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (barley clone Hor3-1 gene Hor3 fragment plus 5'-flanking region fragment)

OTHER NAMES:

CN GenBank X84368

FS NUCLEIC ACID SEQUENCE

SQL 1859

NA 548 a 550 c 462 g 299 t

NTE doublestranded

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     151 gccgattacg cggcttttagc agaccgtcca aaaaaactgt tttgcaaagc
     201 tccaattcct ccttgcttat ccaatttctt ttgtgttggc aaactgcact
     251 tgtccaaccg attttgttct tcccggtgtt cttcttaggc taactaacac
     301 agccgtgcac atagccatgg tccggaatct tcacctcgtc cctataaaag
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1701 gggcaaaaag gatactaccc aagtgcatt tctccgcagc agtcaggaca
1751 aggacaacaa ggataccagc ctagtggagc ttcttcacag gggtcggtgc
1801 aaggggctg ccagcacagc acatcttctc cgcagcagca agcacaaggg
1851 tgccaagct

HITS AT: 435-473

MF Unspecified

CI MAN

SR GenBank

LC STN Files: AGRICOLA, CA, CAPLUS, GENBANK

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L11 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2002 ACS
RN 172866-15-8 REGISTRY
CN DNA (barley D hordein gene promoter region-containing fragment) (9CI)
(CA

INDEX NAME)
FS NUCLEIC ACID SEQUENCE
SQL 2296
NA 629 a 708 c 606 g 353 t

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SEQ      1 caaaactaga gatcaattca ttgacagtcc accgagatgg ctaagcggct
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       151 ctacagtgtg agcgcgagct ccaggagagc tcgctcgagg cgtgccggcg
       201 ggtcgtggac caacagctgg ttggccagct gccatggagc acggggctcc
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ACCESSION NUMBER: 1998:12132 AGRICOLA
DOCUMENT NUMBER: IND20615782
TITLE: Self-incompatibility in the grasses: evolutionary relationship of the S gene from *Phalaris coerulescens* to homologous sequences in other grasses.
AUTHOR(S): Li, X.; Paech, N.; Nield, J.; Hayman, D.; Langridge, P.
CORPORATE SOURCE: University of Adelaide, Glen Osmond.
SOURCE: Plant molecular biology, May 1997. Vol. 34, No. 2. p. 223-232
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412
NOTE: Includes references
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB Self-incompatibility is widespread in the grasses and it is proposed that the grasses share a common incompatibility mechanism that is distinct from those operating in the dicotyledonous species studied in great detail. Where good genetic data are available, all grass species appear to have an

incompatibility mechanism controlled by two unlinked loci, S and Z. A putative S gene has been cloned from *Phalaris coerulescens*. This gene is characterized by two major domains: an allele specificity domain and a **thioredoxin** catalytic domain. A family of sequences with varying degrees of homology to this gene has been identified among 15 grass species covering all subfamilies of the Poaceae. These S-related sequences

appear to be present in the grass family regardless of self-compatibility.

Evidence is presented to show that at least one of the sequences is transcribed, suggesting a functional gene. In contrast to the high expression of the S gene in *Phalaris* pollen, expression of the related gene in the pollen (or anthers) of the grass species examined was so low that RNA gel blot analysis failed to display a significant signal. However, reverse transcription-based polymerase chain reaction (RT-PCR) successfully amplified the region corresponding to the S **thioredoxin** domain from 10 of the grass species. With grasses other than *Phalaris*, RT-PCR showed limited success in amplifying the region corresponding to the S variable portion at the 5' end of the *Phalaris* S gene. Sequencing of the PCR-amplified S **thioredoxin** region from wheat, **barley**, rye and *Dactylis* revealed that this is a highly conserved gene with 94-97% sequence similarity with the corresponding *Phalaris* S gene. The conservation of sequence and ubiquitous expression of the gene across the grass family strongly suggest that the S-related gene is carrying out a significant biological function in the Poaceae. On the basis of these findings, a model for the evolution of the S self-incompatibility gene in the grasses is proposed.